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==============================================================
Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2008; month=1; day=24; hr=14; min=38; sec=20; ms=812; ]
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Application No: 10522513   Version No: 1.0

Input Set:

Output Set:

Started:	2008-01-15 15:36:47.666
Finished:	2008-01-15 15:36:50.863
Elapsed:	0 hr(s) 0 min(s) 3 sec(s) 197 ms
Total Warnings:	52
Total Errors:	0
No. of SeqIDs Defined:	52
Actual SeqID Count:	52

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

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            Input Set:


            Output Set:



            Started:   2008-01-15 15:36:47.666
           Finished:   2008-01-15 15:36:50.863
            Elapsed:   0 hr(s) 0 min(s) 3 sec(s) 197 ms
     Total Warnings:   52
       Total Errors:   0
No. of SeqIDs Defined:  52
   Actual SeqID Count:  52
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Error code	Error Description
	This error has occured more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)

<110>   Brownlie, John
         Chalker, Victoria J.
         Erles, Kerstin

<120>   CANINE RESPIRATORY CORONAVIRUS (CRCV) SPIKE PROTEIN, POLYMERASE AND
HEMAGGLUTININ/ESTERASE

<130>   ERP02.003APC

<140>   10522513
<141>   2008-01-15

<150>   PCT/GB03/02832
<151>   2003-07-01

<150>   GB 0217434.0
<151>   2002-07-27

<160>   52

<170>   PatentIn version 3.1

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<211>   250
<212>   DNA
<213>   canine respiratory coronavirus

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cagctacacg tggtgttcct gttgttatag gcaccactaa attttatggc ggctgggatg   180

atatgttacg tcgccttatt aaagatgttg acaatcctgt acttatgggt tgggattatc   240

ctaagtgtga   250

<210>   2
<211>   83
<212>   PRT
<213>   canine respiratory coronavirus

<400>   2

Gln Met Asn Leu Lys Tyr Ala Ile Ser Ala Lys Asn Arg Ala Arg Thr
1   5   10   15

Val Ala Gly Val Ser Ile Leu Ser Thr Met Thr Gly Arg Met Phe His
            20   25   30

Gln Lys Cys Leu Lys Ser Ile Ala Ala Thr Arg Gly Val Pro Val Val
         35   40   45

Ile Gly Thr Thr Lys Phe Tyr Gly Gly Trp Asp Asp Met Leu Arg Arg
    50   55   60

Leu Ile Lys Asp Val Glu Asn Pro Val Leu Met Gly Trp Asp Tyr Pro
65   70   75   80

Lys Cys Glu

<210>   3
<211>   4092
<212>   DNA
<213>   canine respiratory coronavirus

<400>   3
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gtcgatgtta ctaatggttt aggtacttat tatgtttttag atcgtgtgta tttaaatact   180

acattgttgc ttaatggtta ttatcctact tcaggttcta catatcgtaa tatggcactg   240

aagggaactt tactattgag cacactatgg tttaaaccac catttctttc tgatttttatt   300

gatggtgttt ttgctaaggt aaaaaatacc aaggttatta agatggtgt agtgtatagt   360

gagtttcctg ctataactat aggtagtact tttgtaaata tatcctatag tgtggtagta   420

caaccacata ctactaattt agataataaa ttacaaggtc tcttagagat ctctgtttgc   480

cagtatacta tgtgcgatta cccacatacg atgtgtcatc ctaatctggg taataaacgc   540

atagaactat ggcattggga tacaggtgtt gttccctgtt tatataagcg taatttcaca   600

tatgatgtga atgctgatta tttgtattcc catttttatc aagaaggtgg tactttttat   660

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tgggttacac tctctcacttt taaacaatat ttactcgctt tcaatcaaga tggtgttatt   840

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gatactactg ctacaagttg tcagttgtat tataatttac ctgctagtaa tgtttctatt   1320

agcaggttta atccttctat ttggaatagg agatttggtt ttacagaaca atctgttttt   1380

aagcctcaac ctgtaggtgt ttttactgat catgatgttg tttatgcaca acattgtttt   1440

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aatcatatta tatcattagt gcagaatgct ccatatggtt tgtatttat ccactttagc       3480

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atgcttgttt tactattctt catatgctgt tgtacaggat gtgggactag ttgttttaag       4020

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catgacgact aa                                                          4092


<210>  4
<211>  1363
<212>  PRT
<213>  canine respiratory coronavirus

<400>  4

Met Phe Leu Ile Leu Leu Ile Ser Leu Pro Met Ala Phe Ala Val Ile
1               5                   10                  15
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Gly Asp Leu Lys Cys Thr Thr Val Ser Ile Asn Asp Val Asp Thr Gly
         20   25   30

Ala Pro Ser Ile Ser Thr Asp Val Val Asp Val Thr Asn Gly Leu Gly
         35   40   45

Thr Tyr Tyr Val Leu Asp Arg Val Tyr Leu Asn Thr Thr Leu Leu Leu
     50   55   60

Asn Gly Tyr Tyr Pro Thr Ser Gly Ser Thr Tyr Arg Asn Met Ala Leu
65   70   75   80

Lys Gly Thr Leu Leu Leu Ser Thr Leu Trp Phe Lys Pro Pro Phe Leu
             85   90   95

Ser Asp Phe Ile Asp Gly Val Phe Ala Lys Val Lys Asn Thr Lys Val
         100   105   110

Ile Lys Asp Gly Val Val Tyr Ser Glu Phe Pro Ala Ile Thr Ile Gly
         115   120   125

Ser Thr Phe Val Asn Thr Ser Tyr Ser Val Val Val Gln Pro His Thr
     130   135   140

Thr Asn Leu Asp Asn Lys Leu Gln Gly Leu Leu Glu Ile Ser Val Cys
145   150   155   160

Gln Tyr Thr Met Cys Asp Tyr Pro His Thr Met Cys His Pro Asn Leu
             165   170   175

Gly Asn Lys Arg Ile Glu Leu Trp His Trp Asp Thr Gly Val Val Pro
             180   185   190

Cys Leu Tyr Lys Arg Asn Phe Thr Tyr Asp Val Asn Ala Asp Tyr Leu
         195   200   205

Tyr Ser His Phe Tyr Gln Glu Gly Gly Thr Phe Tyr Ala Tyr Phe Thr
     210   215   220

Asp Thr Gly Val Val Thr Lys Phe Leu Phe His Val Tyr Leu Gly Thr
225   230   235   240

```
Val Leu Ser His Tyr Tyr Val Met Pro Leu Thr Cys Asn Ser Ala Met
            245               250               255


Thr Leu Glu Tyr Trp Val Thr Pro Leu Thr Phe Lys Gln Tyr Leu Leu
            260               265               270


Ala Phe Asn Gln Asp Gly Val Ile Phe Asn Ala Val Asp Cys Lys Ser
            275               280               285


Asp Phe Met Ser Glu Ile Lys Cys Lys Thr Leu Ser Ile Ala Pro Ser
            290               295               300


Thr Gly Val Tyr Glu Leu Asn Gly Tyr Thr Val Gln Pro Ile Ala Asp
305                   310               315                   320


Val Tyr Arg Arg Ile Pro Asn Leu Pro Asp Cys Asn Ile Glu Ala Trp
            325               330               335


Leu Asn Asp Lys Ser Val Pro Ser Pro Leu Asn Trp Glu Arg Lys Thr
            340               345               350


Phe Ser Asn Cys Asn Phe Asn Met Ser Ser Leu Met Ser Phe Ile Gln
            355               360               365


Ala Asp Ser Phe Thr Cys Asn Asn Ile Asp Ala Ala Lys Ile Tyr Gly
            370               375               380


Met Cys Phe Phe Ser Ile Thr Ile Asp Lys Phe Ala Ile Pro Asn Gly
385                   390               395                   400


Arg Lys Val Asp Leu Gln Met Gly Asn Leu Gly Tyr Leu Gln Ser Phe
            405               410               415


Asn Tyr Arg Ile Asp Thr Thr Ala Thr Ser Cys Gln Leu Tyr Tyr Asn
            420               425               430


Leu Pro Ala Ser Asn Val Ser Ile Ser Arg Phe Asn Pro Ser Ile Trp
            435               440               445


Asn Arg Arg Phe Gly Phe Thr Glu Gln Ser Val Phe Lys Pro Gln Pro
450                   455               460


Val Gly Val Phe Thr Asp His Asp Val Val Tyr Ala Gln His Cys Phe
```

```
      465                     470                     475                     480

Lys Ala Pro Thr Asn Phe Cys Pro Cys Lys Leu Asn Gly Ser Leu Cys
                  485                     490                     495


Val Gly Ser Gly Phe Gly Ile Asp Ala Gly Tyr Lys Asn Ser Gly Ile
                  500                     505                     510


Gly Thr Cys Pro Ala Gly Thr Asn Tyr Leu Thr Cys Tyr Asn Ala Asn
                  515                     520                     525


Gln Cys Asp Cys Leu Cys Thr Pro Asp Pro Ile Leu Ser Lys Ser Thr
                  530                     535                     540


Gly Pro Tyr Lys Cys Pro Gln Thr Lys Tyr Leu Val Gly Ile Gly Glu
545                     550                     555                     560


His Cys Ser Gly Leu Ala Ile Lys Ser Asp Tyr Cys Gly Gly Asn Pro
                  565                     570                     575


Cys Thr Cys Gln Pro Lys Ala Phe Leu Gly Trp Ser Val Asp Ser Cys
                  580                     585                     590


Leu Gln Gly Asp Arg Cys Asn Ile Phe Ala Asn Phe Ile Leu His Gly
                  595                     600                     605


Val Asn Ser Gly Thr Thr Cys Ser Thr Asp Leu Gln Lys Ser Asn Thr
                  610                     615                     620


Asp Ile Ile Leu Gly Val Cys Val Asn Tyr Asp Leu Tyr Gly Ile Thr
625                     630                     635                     640


Gly Gln Gly Ile Phe Val Glu Val Asn Ala Thr Tyr Tyr Asn Ser Trp
                  645                     650                     655


Gln Asn Leu Leu Tyr Asp Ser Asn Gly Asn Leu Tyr Gly Phe Arg Asp
                  660                     665                     670


Tyr Leu Thr Asn Arg Thr Phe Met Ile Arg Ser Cys Tyr Ser Gly Arg
                  675                     680                     685


Val Ser Ala Gly Phe His Ser Asn Ser Ser Glu Pro Ala Leu Leu Phe
                  690                     695                     700
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Arg Asn Ile Lys Cys Asn Tyr Val Phe Asn Asn Thr Leu Ser Arg Gln
705   710   715   720

Leu Gln Pro Ile Asn Tyr Phe Asp Ser Tyr Leu Gly Cys Val Val Asn
                725   730   735

Ala Asp Asn Ser Thr Ser Ser Ser Val Gln Thr Cys Asp Leu Thr Val
                740   745   750

Gly Ser Gly Tyr Trp Gly Asp Tyr Ser Thr Gln Arg Arg Ser Arg Arg
            755   760   765

Thr Ile Thr Thr Gly Tyr Arg Phe Thr Asn Phe Glu Pro Phe Thr Val
            770   775   780

Asn Pro Val Asn Asp Ser Leu His Pro Val Gly Gly Leu Tyr Glu Ile
785   790   795   800

Gln Ile Pro Ser Glu Phe Thr Ile Gly Asn Met Glu Glu Phe Ile Gln
                805   810   815

Thr Arg Ser Pro Lys Val Thr Ile Asp Cys Pro Val Phe Val Cys Gly
                820   825   830

Asp Tyr Ala Ala Cys Lys Ser Gln Leu Val Glu Tyr Gly Ser Phe Cys
            835   840   845

Asp Asn Ile Asn Ala Ile Leu Thr Glu Val Asn Glu Leu Leu Asp Thr
            850   855   860

Thr Gln Leu Gln Val Ala Asn Ser Leu Met Asn Gly Val Thr Leu Ser
865   870   875   880

Thr Lys Leu Lys Asp Gly Phe Asn Phe Asn Val Asp Asp Ile Asn Phe
                885   890   895

Ser Pro Val Leu Gly Cys Leu Gly Ser Glu Cys Asn Lys Val Ser Ser
                900   905   910

Arg Ser Ala Ile Glu Asp Leu Leu Phe Ser Lys Val Lys Leu Ser Asp
            915   920   925

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Val Gly Phe Val Asp Ala Tyr Asn Asn Cys Thr Gly Gly Ala Glu Ile
    930                 935                 940


Arg Asp Leu Ile Cys Val Gln Ser Tyr Asn Gly Ile Lys Val Leu Pro
945                 950                 955                 960


Pro Leu Leu Ser Glu Asn Gln Ile Ser Gly Tyr Thr Leu Ala Ala Thr
                965                 970                 975


Phe Ala Ser Leu Phe Pro Pro Trp Ser Ala Ala Ala Gly Val Pro Phe
                980                 985                 990


Tyr Leu Asn Val Gln Tyr Arg Ile  Asn Gly Ile Gly Val  Thr Met Asp
        995                 1000                 1005


Val Leu  Thr Gln Asn Gln Lys  Leu Ile Ser Asn Ala  Phe Asn Asn
    1010                 1015                 1020


Ala Leu  Asp Ala Ile Gln Glu  Gly Phe Asp Ala Thr  Asn Ser Ala
    1025                 1030                 1035


Leu Val  Lys Ile Gln Ala Val  Val Asn Ala Asn Ala  Glu Ala Leu
    1040                 1045                 1050


Asn Asn  Leu Leu Gln Gln Leu  Ser Asn Lys Phe Gly  Ala Ile Ser
    1055                 1060                 1065


Ala Ser  Leu Gln Glu Ile Leu  Ser Arg Leu Asp Ala  Leu Glu Ala
    1070                 1075                 1080


Gln Ala  Gln Ile Asp Arg Leu  Ile Asn Gly Arg Leu  Thr Ala Leu
    1085                 1090                 1095


Asn Ala  Tyr Val Ser Gln Gln  Leu Ser Asp Ser Thr  Leu Val Lys
    1100                 1105                 1110


Phe Ser  Ala Ala Gln Ala Met  Glu Lys Val Asn Glu  Cys Val Lys
    1115                 1120                 1125


Ser Gln  Ser Ser Arg Ile Asn  Phe Cys Gly Asn Gly  Asn His Ile
    1130                 1135                 1140
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```
Ile Ser  Leu Val Gln Asn Ala  Pro Tyr Gly Leu Tyr  Phe Ile His
    1145                1150                1155


Phe Ser  Tyr Val Pro Thr Lys  Tyr Val Thr Ala Lys  Val Ser Pro
    1160                1165                1170


Gly Leu  Cys Ile Ala Gly Asp  Arg Gly Ile Ala Pro  Lys Ser Gly
    1175                1180                1185


Tyr Phe  Val Asn Val Asn Asn  Thr Trp Met Phe Thr  Gly Ser Gly
    1190                1195                1200


Tyr Tyr  Tyr Pro Glu Pro Ile  Thr Gly Asn Asn Val  Val Val Met
    1205                1210                1215


Ser Thr  Cys Ala Val Asn Tyr  Thr Lys Ala Pro Asp  Val Met Leu
    1220                1225                1230


Asn Ile  Ser Thr Pro Asn Leu  Pro Asp Phe Lys Glu  Glu Leu Asp
    1235                1240                1245


Gln Trp
```